SEQUENCE LISTING

<110> Yu et al.

<120> Methods of Treatment of Immune System Related Disorders Using Neutrokine-alpha

<130> PF343P3C4

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Ser Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys
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gag tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc 269
Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser
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Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu
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tct tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa 365
Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln
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ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag 413
Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu
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Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala

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Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly
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cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt      605
Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser
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gaa aca cca act ata caa aaa gga tct tac aca ttt gtt cca tgg ctt      653
Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu
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ctc agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag aat aaa ata      701
Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile
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ttg gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag gtt tta tat      749
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act gat aag acc tac gcc atg gga cat cta att cag agg aag aag gtc      797
Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val
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cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att      845
His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile
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caa aat atg cct gaa aca cta ccc aat aat tcc tgc tat tca gct ggc      893
Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly
    235                 240                 245

att gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca ata cca aga      941
Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg
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gaa aat gca caa ata tca ctg gat gga gat gtc aca ttt ttt ggt gca      989
Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala
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ttg aaa ctg ctg tgacctactt acaccatgtc tgtagctatt ttcctccctt         1041
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Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
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Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
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Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65                  70                  75                  80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
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Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
            100                 105                 110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
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Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
    130                 135                 140

Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
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Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
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Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
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Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
        195                 200                 205

Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
    210                 215                 220

Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225                 230                 235                 240

Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
                245                 250                 255

Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
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Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
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Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
         35                  40                  45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
     50                  55                  60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
 65                  70                  75                  80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
                 85                  90                  95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
            100                 105                 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
        115                 120                 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
    130                 135                 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145                 150                 155                 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
                165                 170                 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
            180                 185                 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
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Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
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Gln Val Tyr Phe Gly Ile Ile Ala Leu
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Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
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Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
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 65                  70                  75                  80

Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
                 85                  90                  95

Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
            100                 105                 110

Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro
        115                 120                 125

Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
    130                 135                 140

His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
145                 150                 155                 160

Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
                165                 170                 175

Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
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Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
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Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
        35                  40                  45

Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln
     50                  55                  60

Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu
 65                  70                  75                  80

Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
                 85                  90                  95

Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
            100                 105                 110

Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro
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        115                 120                 125

Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg
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Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg
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Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu
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Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala
            180                 185                 190

Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly
        195                 200                 205

Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser
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Val Met Val Gly
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Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
         35                  40                  45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
     50                  55                  60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
 65                  70                  75                  80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
                 85                  90                  95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
            100                 105                 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
        115                 120                 125
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C1 cont

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Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
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Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
145                 150                 155                 160

Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
                165                 170                 175

Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
            180                 185                 190

Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
        195                 200                 205

His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
    210                 215                 220

Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
225                 230                 235                 240

Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
                245                 250                 255

Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
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Gln Thr Phe Phe Gly Leu Tyr Lys Leu
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ttgccttaag aaaagagaag aaatgaaact gnaaggagtg tgtttccatc ctcccacgga 240
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tgctattcag ctggcattgc aaaactggna ggaaggagat gaactccaac ttgcaatacc 240
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ctggggctgc tcctggtgtt gcctgctgcc ttccctgccc cagttgtgag acaaggggac 120
ctggccagc 129

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 17
gtgggatcct tacagcagtt tcaatgcacc 30

<210> 18
<211> 903
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(798)

<400> 18
atg gat gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt 48
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
1 5 10 15

aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 96
Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30

cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 144
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35 40 45

gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 192
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50 55 60

tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg 240
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65 70 75 80

gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 288
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
85 90 95

gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg 336
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
100 105 110

C1 Cont

aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac 384
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
115 120 125

agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gga tct tac 432
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
130 135 140

aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa 480
Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
145 150 155 160

gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata 528

```
Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile
                165                 170                 175

tat ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat cta   576
Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu
            180                 185                 190

att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg   624
Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val
        195                 200                 205

act ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat aat   672
Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn
    210                 215                 220

tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc   720
Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu
225                 230                 235                 240

caa ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga gat   768
Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp
                245                 250                 255

gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt acaccatgtc     818
Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
            260                 265

tgtagctatt ttcctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac 878

caaaaaaaaa aaaaaaaaaa aaaaa                                       903


<210> 19
<211> 266
<212> PRT
<213> Homo sapiens

<400> 19
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
  1               5                  10                  15

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
             20                  25                  30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
         35                  40                  45

Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
     50                  55                  60

Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 65                  70                  75                  80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
                 85                  90                  95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
            100                 105                 110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
```

C1 Cont

```
        115                 120                 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
    130                 135                 140

Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
145                 150                 155                 160

Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile
                165                 170                 175

Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu
            180                 185                 190

Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val
        195                 200                 205

Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn
    210                 215                 220

Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu
225                 230                 235                 240

Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp
                245                 250                 255

Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
            260                 265
```

<210> 20
<211> 136
<212> PRT
<213> Homo sapiens

<400> 20

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His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp
  1               5                  10                  15

Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg
             20                  25                  30

Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val
         35                  40                  45

Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met
     50                  55                  60

Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe
 65                  70                  75                  80

Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
                85                  90                  95

Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser
            100                 105                 110

Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly
        115                 120                 125
```

C1 Cont

```
Thr Phe Leu Gly Phe Val Lys Leu
    130                 135
```

<210> 21
<211> 462
<212> DNA
<213> Homo sapiens

<400> 21
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atggctgttc agggtccgga agaaaccgtt actcaggact gccttcagct gatcgcagac 60
tctgaaactc cgaccatcca gaaaggttct tacacctttg ttccttggct gctttctttc 120
aaacgtggtt ctgccctgga agagaaagaa aacaaaatcc tggttaaaga aactggttac 180
ttctttatct acggtcaggt tctttacact gataagacct acgccatggg tcacctgatt 240
cagcgtaaga aagttcacgt tttcggtgac gagctgtctc tggttactct gtttcgctgc 300
attcagaaca tgccggaaac tcttcctaac aactcctgct actctgctgg catcgcaaaa 360
ctggaagagg gtgatgaact gcagctggca attcctcgtg aaaacgcaca aatttctctg 420
gacggtgatg taaccttctt tggtgcactg aaacttctgt aa                    462
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<210> 22
<211> 1040
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(468)

<400> 22
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cgc gtg gta gac ctc tca gct cct cct gca cca tgc ctg cct gga tgc   48
Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
  1               5                  10                  15

cgc cat tct caa cat gat gat aat gga atg aac ctc aga aac aga act   96
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
             20                  25                  30

tac aca ttt gtt cca tgg ctt ctc agc ttt aaa aga gga aat gcc ttg   144
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
         35                  40                  45

gag gag aaa gag aac aaa ata gtg gtg agg caa aca ggc tat ttc ttc   192
Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
     50                  55                  60

atc tac agc cag gtt cta tac acg gac ccc atc ttt gct atg ggt cat   240
Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
 65                  70                  75                  80

gtc atc cag agg aag aaa gta cac gtc ttt ggg gac gag ctg agc ctg   288
Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
                 85                  90                  95

gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac   336
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
            100                 105                 110

aat tcc tgc tac tcg gct ggc atc gcg agg ctg gaa gaa gga gat gag   384
```

C' cont

```
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
        115                 120                 125

att cag ctt gca att cct cgg gag aat gca cag att tca cgc aac gga   432
Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
    130                 135                 140

gac gac acc ttc ttt ggt gcc cta aaa ctg ctg taa ctcacttgct        478
Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
145                 150                 155

ggagtgcgtg atccccttcc ctcgtcttct ctgtacctcc gagggagaaa cagacgactg 538

gaaaaactaa aagatgggga aagccgtcag cgaaagtttt ctcgtgaccc gttgaatctg 598

atccaaacca ggaaatataa cagacagcca caaccgaagt gtgccatgtg agttatgaga 658

aacggagccc gcgctcagaa agaccggatg aggaagaccg ttttctccag tcctttgcca 718

acacgcaccg caaccttgct ttttgccttg ggtgacacat gttcagaatg cagggagatt 778

tccttgtttt gcgatttgcc atgagaagag ggcccacaac tgcaggtcac tgaagcattc 838

acgctaagtc tcaggattta ctctcccttc tcatgctaag tacacacacg ctcttttcca 898

ggtaatacta tgggatacta tggaaaggtt gtttgttttt aaatctagaa gtcttgaact 958

ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata aacttaatta aaaaggttta 1018

agtgtgaaaa aaaaaaaaaa aa                                          1040


<210> 23
<211> 155
<212> PRT
<213> Homo sapiens

<400> 23
Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
  1               5                  10                  15
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
            20                  25                  30
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
        35                  40                  45
Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
    50                  55                  60
Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
65                  70                  75                  80
Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
                85                  90                  95
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
            100                 105                 110
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
        115                 120                 125
Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
    130                 135                 140
Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
145                 150                 155
```

C1 Cont

<210> 24
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 24
ccaccagctc caggagaagg caactc 26

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 25
accgcgggac tgaaaatct 19

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 26
cacgcttatt tctgctgttc tga 23

<210> 27
<211> 657
<212> DNA
<213> Homo sapiens

<400> 27
taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagggccac 60
cacgcggaga agctgccagc aagagcaaga gcccccaagg ccggtctggg ggaagctcca 120
gctgtcaccg caggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcat tcaagactgc 240
ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttgtt 300
ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
gtcaaagaaa ctggttactt ttttatatat ggtcaggttt tatacactga taagacctat 420
gccatgggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagtctg 480
gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac tacccaataa ttcctgctat 540
tcagctggca ttgcaaaact ggaagaagga gatgaacttc aacttgcaat accacgagaa 600
aatgcacaaa tatcactgga tggagatgtc acatttttg gtgccctcaa actgctg 657

C1 cont

<210> 28
<211> 219

<212> PRT
<213> Homo sapiens

<400> 28
Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
1 5 10 15

Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
20 25 30

Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
35 40 45

Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
50 55 60

Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
65 70 75 80

Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
85 90 95

Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
100 105 110

Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
115 120 125

Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
130 135 140

Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
145 150 155 160

Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
165 170 175

Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
180 185 190

Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
195 200 205

Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
210 215

C1 Cont

<210> 29
<211> 657
<212> DNA
<213> Homo sapiens

<400> 29
taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagagccac 60
cacgcggaga agctgccagc aagagcaaga gcccccaagg ccggtctggg ggaagctcca 120
gctgtcaccg cgggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcat tcaagactgc 240
ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttgtt 300
ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
gtcaaagaaa ctggttactt ttttatatat ggtcaggttt tatacactga taagacctat 420

gccatgggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagtctg 480
gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac tacccaataa ttcctgctat 540
tcagctggca ttgcaaaact ggaagaaggg gatgaacttc aacttgcaat accacgagaa 600
aatgcacaaa tatcactgga tggagatgtc acatttttg gtgccctcaa actgctg 657

<210> 30
<211> 219
<212> PRT
<213> Homo sapiens

<400> 30
Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
1 5 10 15

Leu Gln Ser His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
20 25 30

Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
35 40 45

Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
50 55 60

Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
65 70 75 80

Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
85 90 95

Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
100 105 110

Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
115 120 125

Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
130 135 140

Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
145 150 155 160

Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
165 170 175

C1 CONT

Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
180 185 190

Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
195 200 205

Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
210 215

<210> 31
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 31
ggtcgccgtt tctaacgcgg ccgttcaggg tccagaag 38

<210> 32
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 32
ctggttcggc ccaaggtacc aagcttgtac cttagatctt ttctagatc 49

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 33
ctggtagttc ttcggagtgt g 21

<210> 34
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 34
cgcgttagaa acggcgacc 19

C1 Cont

<210> 35
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<220>
<221> misc_feature
<222> (7)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (12)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (16)
<223> n equals deoxyinosine

<400> 35
taccagntgg cngccntgca ag 22

<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<220>
<221> misc_feature
<222> (3)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (14)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (16)..(17)
<223> n equals deoxyinosine

<400> 36
gtnacagcag tttnanngca cc 22

C1 Cont

<210> 37
<211> 866
<212> DNA
<213> Mus musculus

<400> 37
atggatgagt ctgcaaagac cctgccacca ccgtgcctct gtttttgctc cgagaaagga 60
gaagatatga aagtgggata tgatcccatc actccgcaga aggaggaggg tgcctggttt 120
gggatctgca gggatggaag gctgctggct gctaccctcc tgctggccct gttgtccagc 180
agtttcacag cgatgtcctt gtaccagttg gctgccttgc aagcagacct gatgaacctg 240
cgcatggagc tgcagagcta ccgaggttca gcaacaccag ccgccgcggg tgctccagag 300
ttgaccgctg gagtcaaact cctgacaccg gcagctcctc gaccccacaa ctccagccgc 360
ggccacagga acagacgcgc cttccaggga ccagaggaaa cagaacaaga tgtagacctc 420
tcagctcctc ctgcaccatg cctgcctgga tgccgccatt ctcaacatga tgataatgga 480
atgaacctca gaaacatcat tcaagactgt ctgcagctga ttgcagacag cgacacgccg 540
gccttggagg agaaagagaa caaaatagtg gtgaggcaaa caggctattt cttcatctac 600
agccaggttc tatacacgga ccccatcttt gctatgggtc atgtcatcca gaggaagaaa 660

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gtacacgtct ttggggacga gctgagcctg gtgaccctgt tccgatgtat tcagaatatg 720
cccaaaacac tgcccaacaa ttcctgctac tcggctggca tcgcgaggct ggaagaagga 780
gatgagattc agcttgcaat tcctcgggag aatgcacaga tttcacgcaa cggagacgac 840
accttctttg gtgccctaaa actgct                                      866
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<210> 38
<211> 289
<212> PRT
<213> Mus musculus

<400> 38

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Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
  1               5                  10                  15

Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
             20                  25                  30

Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
         35                  40                  45

Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
     50                  55                  60

Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
 65                  70                  75                  80

Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
                 85                  90                  95

Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
            100                 105                 110

Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
        115                 120                 125

Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
    130                 135                 140

Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
145                 150                 155                 160

Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
                165                 170                 175

Ser Asp Thr Pro Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg
            180                 185                 190

Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro
        195                 200                 205

Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe
    210                 215                 220

Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met
225                 230                 235                 240

Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg
                245                 250                 255
```

Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala
260 265 270

Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu
275 280 285

Leu

<210> 39
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 39
cagactggat ccgccaccat ggatgactcc acagaaag 38

<210> 40
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 40
cagactggta ccgtcctgcg tgcactacat ggc 33

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 41
tggtgtcttt ctaccaggtg g 21

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer

<400> 42
tttcttctgg accctgaacg g 21